

SEQUENCE LISTING

(1) GENERAL INFORMATION:

15 (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(ii) TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING DENDRITIC CELL-T CELL INTERACTION

25 (iii) NUMBER OF SEQUENCES: 2

(2) INFORMATION FOR SEQ ID NO:1:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear.

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

40 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

45 ATGAGTGACT CCAAGGAACC AAGACTGCAG CAGCTGGGCC TCCTGGAGGA GGAACAGCTG 60
 AGAGGCCCTTG GATTCCGACA GACTCGAGGA TACAAGAGCT TAGCAGGGTG TCTTGGCCAT 120
 GGTCCCCCTGG TGCTGCAACT CCTCTCCTTC ACGCTCTTGG CTGGGCTCCT TGTCCAAGTG 180
 50 TCCAAGGTCC CCAGCTCCAT AAGTCAGGAA CAATCCAGGC AAGACGCGAT CTACCAGAAC 240
 CTGACCCAGC TTAAAGCTGC AGTGGGTGAG CTCTCAGAGA AATCCAAGCT GCAGGAGATC 300
 55 TACCAGGAGC TGACCCAGCT GAAGGCTGCA GTGGGTGAGC TTCCAGAGAA ATCTAAGCTG 360

	CAGGAGATCT ACCAGGAGCT GACCCGGCTG AAGGCTGCAG TGGGTGAGCT TCCAGAGAAA	420
5	TCTAAGCTGC AGGAGATCTA CCAGGAGCTG ACCTGGCTGA AGGCTGCAGT GGGTGAGCTT	480
	CCAGAGAAAT CTAAGATGCA GGAGATCTAC CAGGAGCTGA CTCGGCTGAA GGCTGCAGTG	540
10	GGTGAGCTTC CAGAGAAATC TAAGCAGCAG GAGATCTACC AGGAGCTGAC CGGGCTGAAG	600
	GCTGCAGTGG GTGAGCTTCC AGAGAAATCT AAGCAGCAGG AGATCTACCA GGAGCTGACC	660
	CGGCTGAAGG CTGCAGTGGG TGAGCTTCCA GAGAAATCTA AGCAGCAGGA GATCTACCA	720
15	GAGCTGACCC AGCTGAAGGC TGCA GTGGAA CGCCTGTGCC ACCCCTGTCC CTGGGAATGG	780
	ACATTCTTCC AAGGAAACTG TTACTTCATG TCTAACTCCC AGCGGAAC TG GCACGACTCC	840
	ATCACCGCCT GCAAAGAAGT GGGGGCCAG CTCGTCGTA TCAAAAGTGC TGAGGAGCAG	900
20	AACTTCCTAC AGCTGCAGTC TTCCAGAAGT AACCGCTTCA CCTGGATGGG ACTTTAGAT	960
	CTAAATCAGG AAGGCACGTG GCAATGGGTG GACGGCTCAC CTCTGTTGCC CAGCTTCAAG	1020
	CAGTATTGGA ACAGAGGAGA GCCCAACAAC GTTGGGGAGG AAGACTGCGC GGAATTTAGT	1080
25	GGCAATGGCT GGAACGACGA CAAATGTAAT CTTGCCAAAT TCTGGATCTG CAAAAAGTCC	1140
	GCAGCCTCCT GCTCCAGGGA TGAAGAACAG TTCTTCTC CAGCCCCCTGC CACCCCAAAC	1200
30	CCCCCTCCTG CGTAG	1215

2) INFORMATION FOR SEQ ID NO:2:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

45	Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu	
	1 5 10 15	
	Glu Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly	
	20 25 30	
50	Tyr Lys Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu	
	35 40 45	
	Gln Leu Leu Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val	
55	50 55 60	

Ser Lys Val Pro Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp
65 70 75
Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly Glu
80 85 90
Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
95 100 105
10 Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu
110 115 120
Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly
125 130 135
15 Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu
140 145 150
Thr Trp Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys
20 155 160 165
Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val
170 175 180
25 Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu
185 190 195
Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser
200 205 210
30 Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala
215 220 225
Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln
35 230 235 240
Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro
245 250 255
40 Cys Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met
260 265 270
Ser Asn Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys
275 280 285
45 Glu Val Gly Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln
290 295 300
50 Asn Phe Leu Gln Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp
305 310 315
Met Gly Leu Ser Asp Leu Asn Gln Glu Gly Thr Trp Gln Trp Val
320 325 330
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Asp Gly Ser Pro Leu Leu Pro Ser Phe Lys Gln Tyr Trp Asn Arg
335 340 345
Gly Glu Pro Asn Asn Val Gly Glu Glu Asp Cys Ala Glu Phe Ser
5 350 355 360
Gly Asn Gly Trp Asn Asp Asp Lys Cys Asn Leu Ala Lys Phe Trp
365 370 375
10 Ile Cys Lys Lys Ser Ala Ala Ser Cys Ser Arg Asp Glu Glu Gln
380 385 390
Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn Pro Pro Pro Ala *
15 395 400 404